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Abbruzzo, Antonio

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Stellingen
behorende bij het proefschrift
Graphical models for estimating dynamic networks

door
Antonino Abbruzzo

- I. A genomic network is only a metaphor for genetic regulation and signalling (Chapter 1).
- II. Graphical models are only one formalization of a network, albeit a powerful one (Chapter 2).
- III. Colouring graphs is fun, but computationally difficult (Chapter 3).
- IV. Sparsity is not only computationally useful, but also represents our current best knowledge of genomic interaction (Chapter 2).
- V. Networks are too often seen as state entities. The overall aim of this thesis is to animate them (Chapter 3-5).
- VI. Popularly, interactions are seen as first moment properties. Surprisingly, Gaussian graphical models show that it is easier to implement them via second moments (Chapter 2).
- VII. On the side of having destroyed many pension plans, the Gaussian Copula is particularly useful for dealing with non-normal genomic data (Chapter 4).
- VIII. Our biology is resistant to change both neurologically as well as genetically. That is why in (Chapter 5.1) we like the model that infer only slowly changing genomic networks.
- IX. Scale-free networks are obviously rubbish models for the genomic reality, but can serve as prior for doing inference (Chapter 5.2).
- X. "....."
(Non-observed information make inference a lot harder) (Chapter 5.3).